

#9



PCT09

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/581,770

DATE: 02/20/2003

TIME: 14:41:42

Input Set : A:\1.txt

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5 <110> APPLICANT: K. Sampath et al.
 7 <120> TITLE OF INVENTION: METHODS FOR MAINTAINING OR RESTORING TISSUE-APPROPRIATE
 PHENOTYPE OF
 8 SOFT TISSUE CELLS
 10 <130> FILE REFERENCE: CIBT-P01-520
 12 <140> CURRENT APPLICATION NUMBER: 09/581,770
 13 <141> CURRENT FILING DATE: 2000-12-29
 15 <150> PRIOR APPLICATION NUMBER: PCT/US98/26788
 16 <151> PRIOR FILING DATE: 1998-12-16
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1067
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Mus musculus
 27 <400> SEQUENCE: 1
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 30 acacggatgg agaccatggt tattttctttg ggagaaaagc ctaattggga cgcttcgaga 120
 32 tccctatagg aaattgcacc agtagtcaac tggattttta aaaggcaaag cttgaggatt 180
 34 tttttttccc ttgaaatga atgtagcaaa cttatgtaag cacggaatag gattattagt 240
 36 taacagtctt ttcaattata tgggaaaatg aaaactaggg gagcgtctaa ggccacttgc 300
 38 tgacctttgt gcagctgtta agtaaagaaa gtaaaccctc cagggatact gaacagccaa 360
 40 ctgtcataag tccaggggtgt cttgcacttg ctgtgacaag tttaaaatat ttaatatgac 420
 42 tatacctgaa atattttaatg ctatcttttt catgcaccag cttctaagag ctttccctaa 480
 44 aatcctgata tgcaaaagaa tataccaata ttttccccct tgcccctggc gcttgtctcc 540
 46 caagtttagca aacacttagg taagcgattt ttacagaact tttttcccta ataactgaag 600
 48 gactaacatg atgatttaga tctatatctt ccccaaaaagg cgtctcatat ttttgtatat 660
 50 taccaaatat tttcagtc aaataacacaag aatgtatttt aaaaataaaa aggggtgaatc 720
 52 atcattccat catgaaccaa cattggagtc agaactccta aaaggaaaac agaaaaaaaa 780
 54 aaaaaaatcat gcacagccga agctattaat atataatgga gacaaagagt ttatttttca 840
 56 atgagaataa caaggaaaaa agcctgattt tgtacgcctg cccgttagga cttcccacca 900
 58 taatttagtgc ttcttgcccc tgagaggagg agcttcggct caggggaact tcatgcaata 960
 60 agggaagaaa acagtataaa tactccaggg cagccgtggg gaaggcatta tccactgctc 1020
 62 ctgggcagag gaagccagga aagctgcccc acgcatctcc cagcacc 1067
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 65 <211> LENGTH: 21
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial Sequence
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: AP1 sequence A
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 73 cgcttgatga ctcagccgga a 21
 75 <210> SEQ ID NO: 3
 76 <211> LENGTH: 10

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77 <212> TYPE: DNA
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80 <220> FEATURE:
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84 ttcctcatca 10
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94 1 5 10 15
97 Arg Ile Arg Asn Lys Met Ala Ala Ala
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117 <220> FEATURE:
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128 <220> FEATURE:
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130 <222> LOCATION: (49)..(1341)
131 <223> OTHER INFORMATION:
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134 ggtgcgggcc cggagcccgg agcccgggta ggcgcgtagag ccggcgcg atg cac gtg 57
135 Met His Val
136 1
138 cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105
139 Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
140 5 10 15
142 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
143 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
144 20 25 30 35

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146	gag	gtg	cac	tcg	agc	ttc	atc	cac	cgg	cgc	ctc	cgc	agc	cag	gag	cgg	201
147	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	Gln	Glu	Arg	
148				40					45					50			
150	cgg	gag	atg	cag	cgc	gag	atc	ctc	tcc	att	ttg	ggc	ttg	ccc	cac	cgc	249
151	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg	
152				55					60					65			
154	ccg	cgc	ccg	cac	ctc	cag	ggc	aag	cac	aac	tcg	gca	ccc	atg	ttc	atg	297
155	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	
156				70				75					80				
158	ctg	gac	ctg	tac	aac	gcc	atg	gcg	gtg	gag	gag	ggc	ggc	ggg	ccc	ggc	345
159	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	Gly	Pro	Gly	
160		85					90					95					
162	ggc	cag	ggc	ttc	tcc	tac	ccc	tac	aag	gcc	gtc	ttc	agt	acc	cag	ggc	393
163	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	
164	100						105				110				115		
166	ccc	cct	ctg	gcc	agc	ctg	caa	gat	agc	cat	ttc	ctc	acc	gac	gcc	gac	441
167	Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
168					120					125				130			
170	atg	gtc	atg	agc	ttc	gtc	aac	ctc	gtg	gaa	cat	gac	aag	gaa	ttc	ttc	489
171	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
172					135					140				145			
174	cac	cca	cgc	tac	cac	cat	cga	gag	ttc	cgg	ttt	gat	ctt	tcc	aag	atc	537
175	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
176				150				155					160				
178	cca	gaa	ggg	gaa	gct	gtc	acg	gca	gcc	gaa	ttc	cgg	atc	tac	aag	gac	585
179	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
180		165					170					175					
183	tac	atc	cgg	gaa	cgc	ttc	gac	aat	gag	acg	ttc	cgg	atc	agc	gtt	tat	633
184	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
185	180						185				190				195		
187	cag	gtg	ctc	cag	gag	cac	ttg	ggc	agg	gaa	tcg	gat	ctc	ttc	ctg	ctc	681
188	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
189					200					205				210			
191	gac	agc	cgt	acc	ctc	tgg	gcc	tcg	gag	gag	ggc	tgg	ctg	gtg	ttt	gac	729
192	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
193				215					220				225				
195	atc	aca	gcc	acc	agc	aac	cac	tgg	gtg	gtc	aat	ccg	cgg	cac	aac	ctg	777
196	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
197				230				235					240				
199	ggc	ctg	cag	ctc	tcg	gtg	gag	acg	ctg	gat	ggg	cag	agc	atc	aac	ccc	825
200	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
201		245					250					255					
203	aag	ttg	gcg	ggc	ctg	att	ggg	cgg	cac	ggg	ccc	cag	aac	aag	cag	ccc	873
204	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
205	260						265				270				275		
207	ttc	atg	gtg	gct	ttc	aag	gcc	acg	gag	gtc	cac	ttc	cgc	agc	atc		921
208	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	
209					280					285				290			
211	cgg	tcc	acg	ggg	agc	aaa	cag	cgc	agc	cag	aac	cgc	tcc	aag	acg	ccc	969

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212 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
213          295          300          305
215 aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc      1017
216 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
217          310          315          320
219 agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc      1065
220 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
221          325          330          335
223 cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc      1113
224 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
225 340          345          350          355
227 gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg      1161
228 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
229          360          365          370
231 aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac      1209
232 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
233          375          380          385
235 ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc      1257
236 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
237          390          395          400
239 atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa      1305
240 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
241          405          410          415
244 tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc      1351
245 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
246 420          425          430
248 gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag      1411
250 gaaccagcag accaactgcc ttttgtgaga ccttcccctc cctatcccca actttaaagg      1471
252 tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc      1531
254 atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaac      1591
256 gcataaagaa aaatggccgg gccaggtcac tggctgggaa gtctcagcca tgcacggact      1651
258 cgtttccaga ggtaattatg agcgccctacc agccaggcca ccagccgtg ggaggaagg      1711
260 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc      1771
262 ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaa aaaaaaaaaa a      1822
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267 <211> LENGTH: 431
269 <212> TYPE: PRT
271 <213> ORGANISM: Homo sapiens
275 <400> SEQUENCE: 8
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281 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
282          20          25          30
285 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
286          35          40          45
289 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
290          50          55          60
293 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
294 65          70          75          80

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297 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
298      85                      90                      95
301 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
302      100                      105                      110
305 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
306      115                      120                      125
309 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
310      130                      135                      140
313 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
314 145                      150                      155                      160
317 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
318      165                      170                      175
321 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
322      180                      185                      190
325 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
326      195                      200                      205
329 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
330      210                      215                      220
333 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
334 225                      230                      235                      240
337 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
338      245                      250                      255
341 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
342      260                      265                      270
345 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
346      275                      280                      285
349 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
350      290                      295                      300
353 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
354 305                      310                      315                      320
357 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
358      325                      330                      335
361 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
362      340                      345                      350
366 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
367      355                      360                      365
370 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
371      370                      375                      380
374 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
375 385                      390                      395                      400
378 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
379      405                      410                      415
382 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
383      420                      425                      430

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VERIFICATION SUMMARY

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